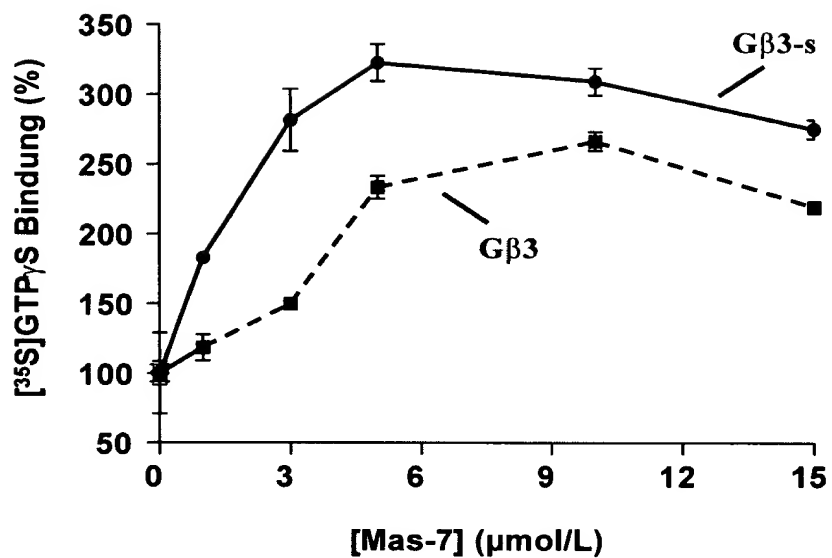


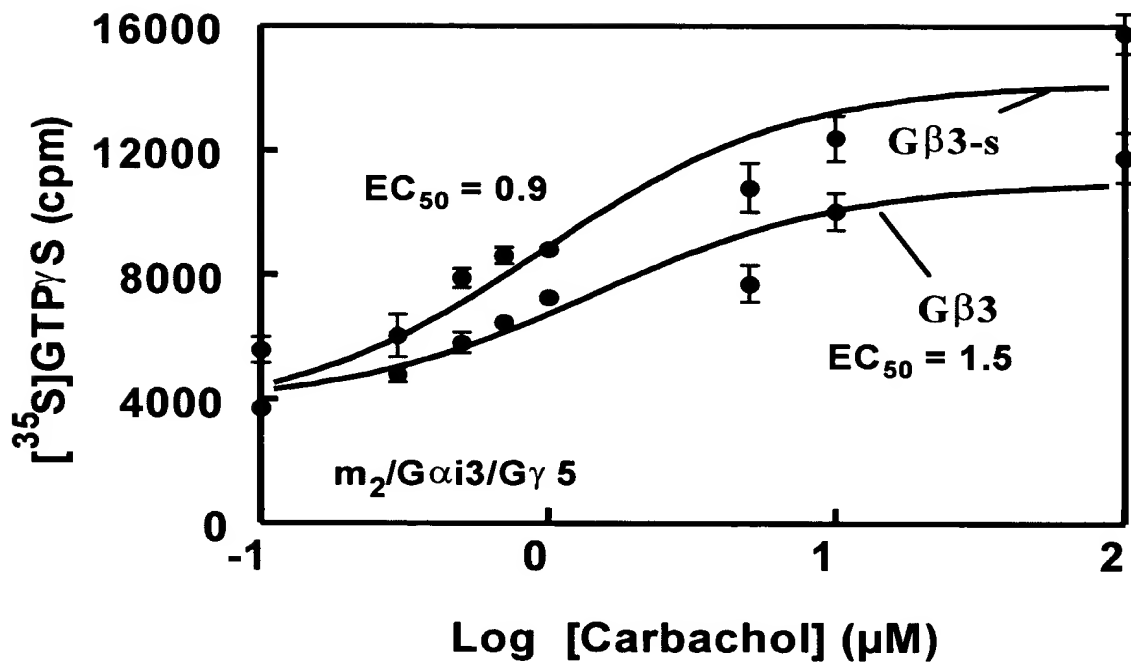


FIG. 1



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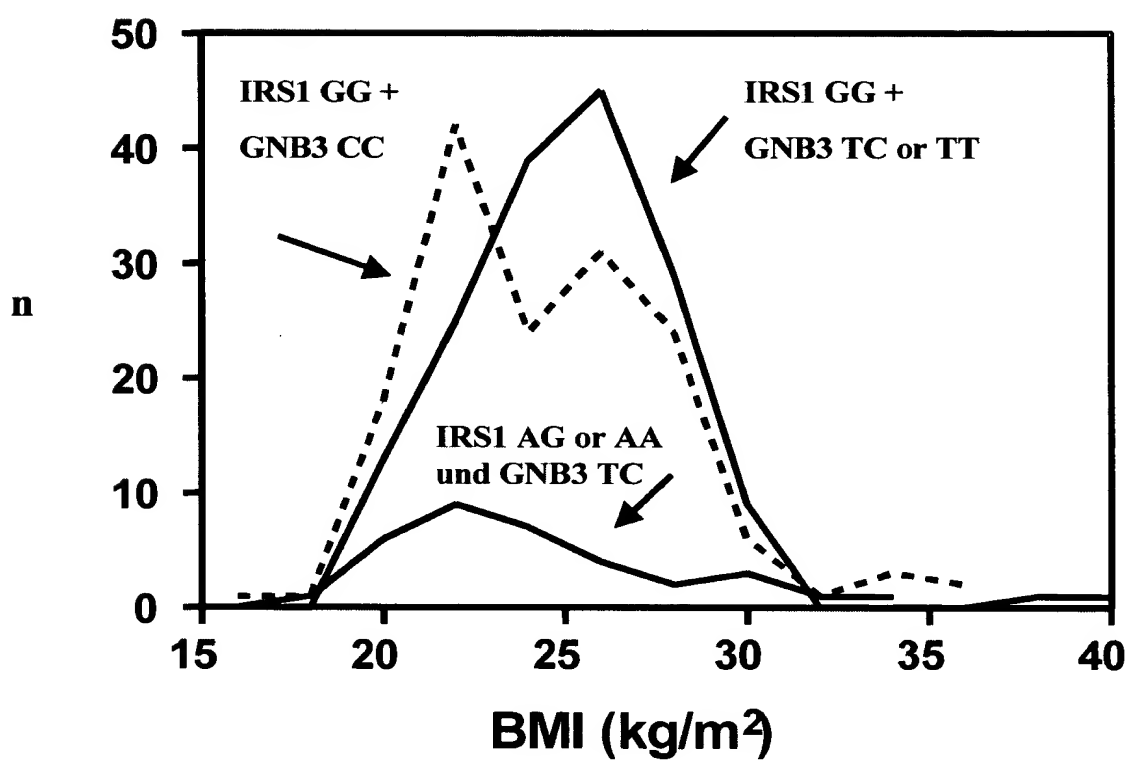
FIG. 2





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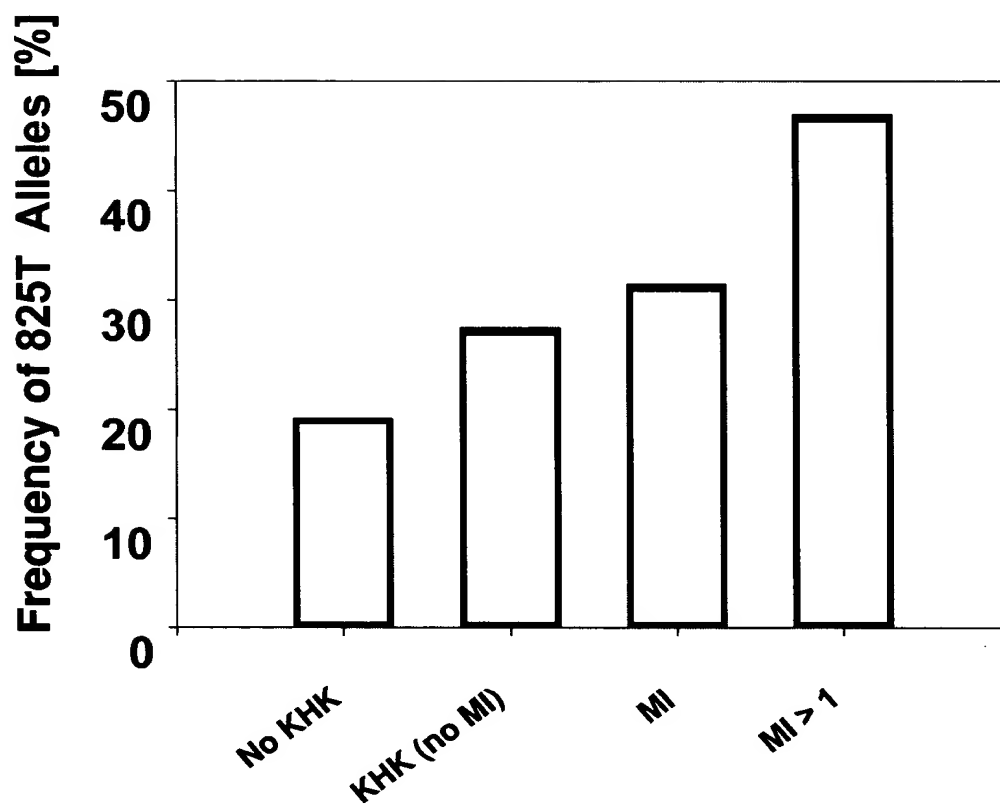
FIG. 3





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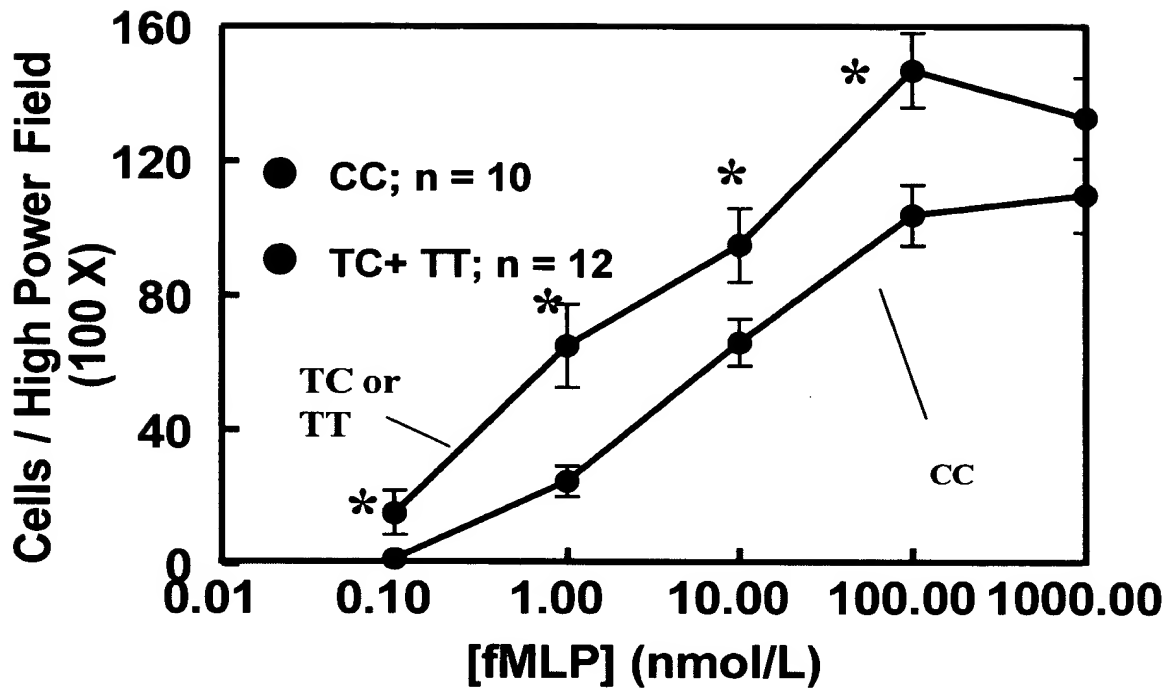
FIG. 4





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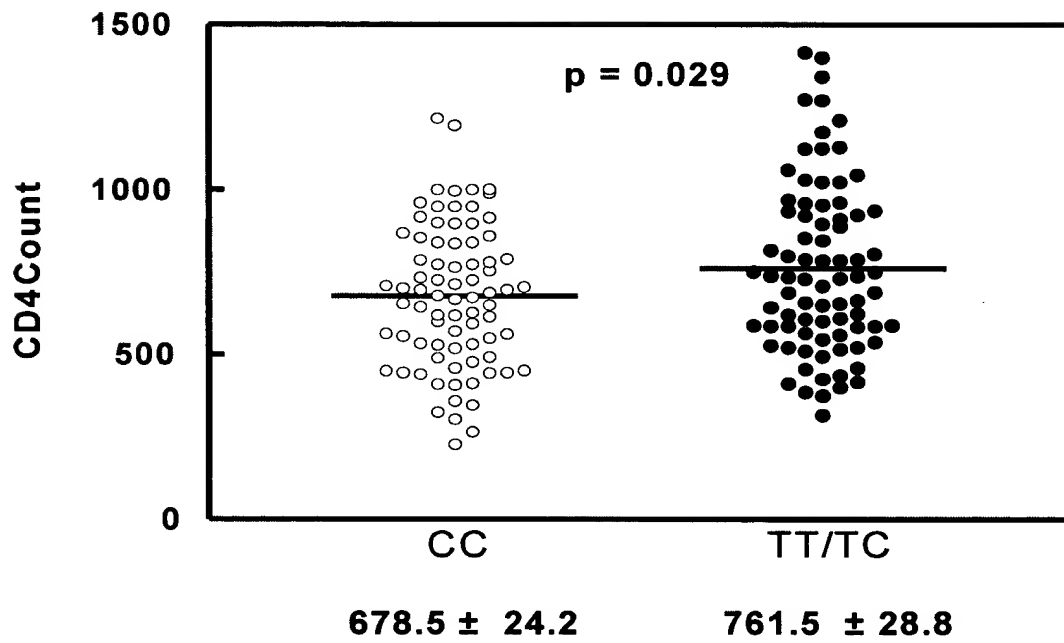
FIG. 5





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FIG. 6

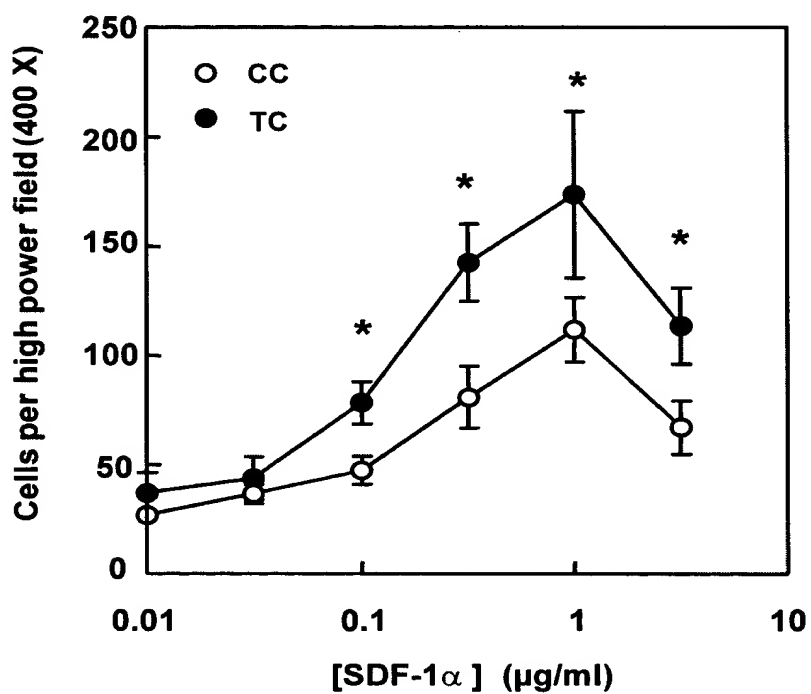




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FIG. 7

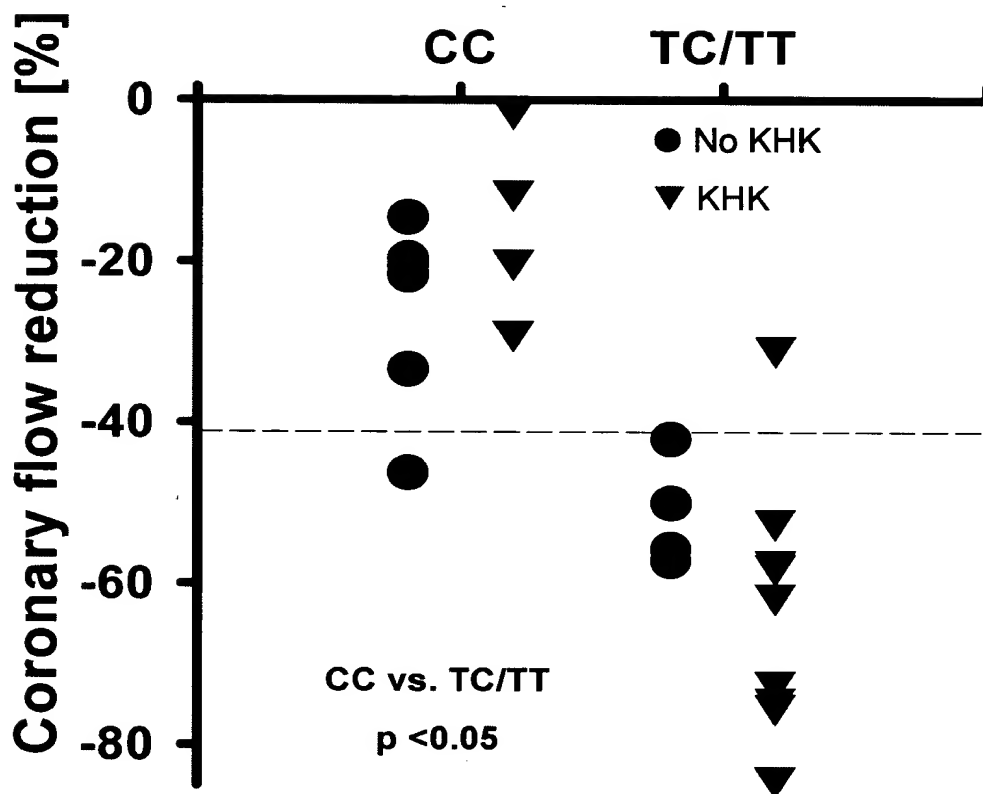
**Enhanced Chemotaxis of T-Lymphocytes from  
825T Allele Carriers**





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FIG. 8





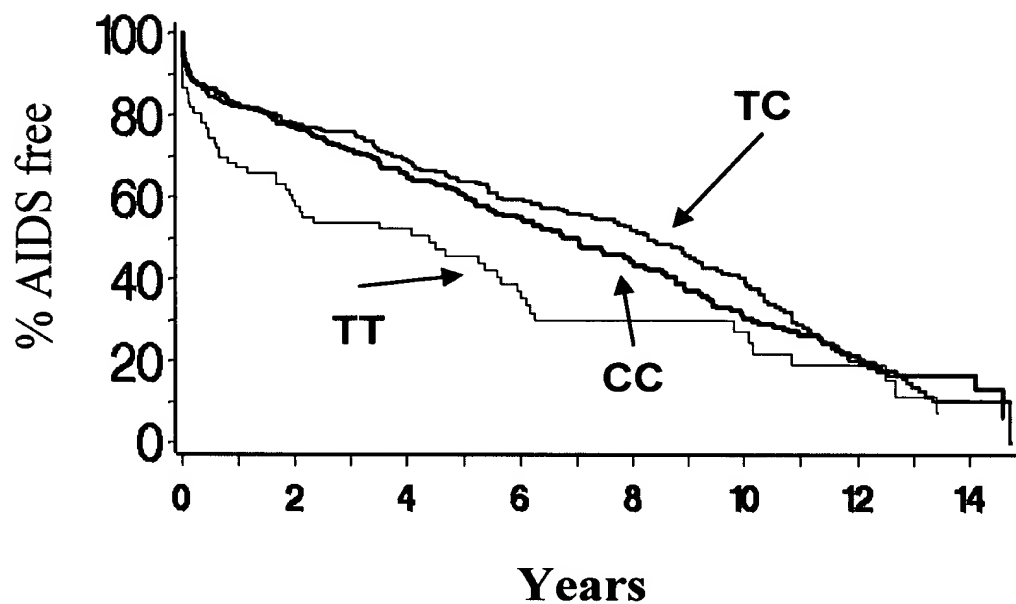


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FIG. 9

### Time to AIDS

AIDS is defined as AIDS-defining disorders or CD4 count < 200

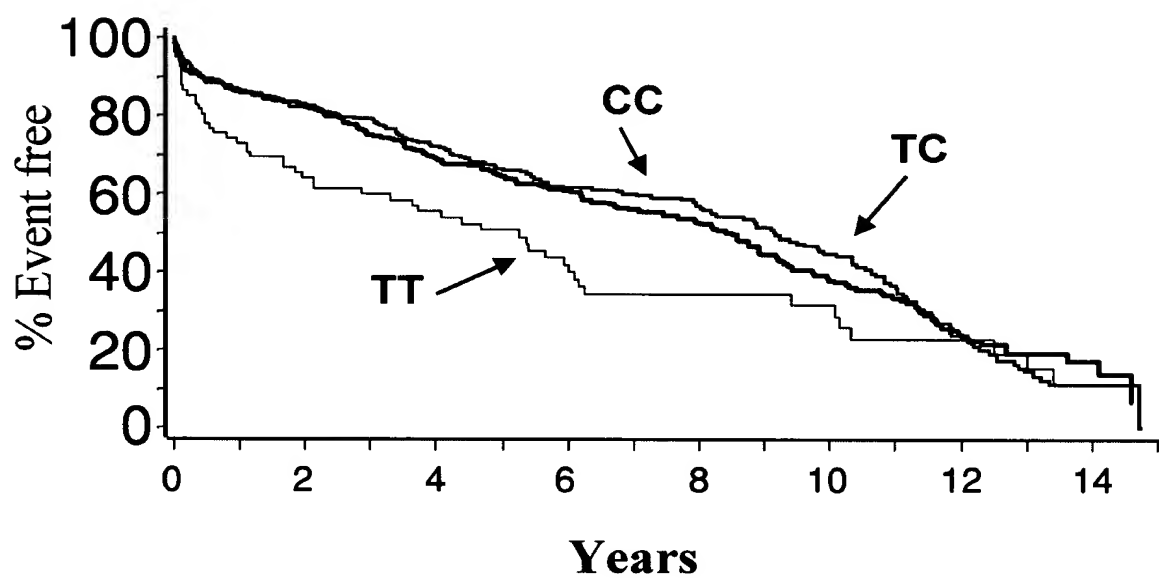




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FIG. 10

**Event: CD4 Cell Count Below 200 per  $\mu$ l**

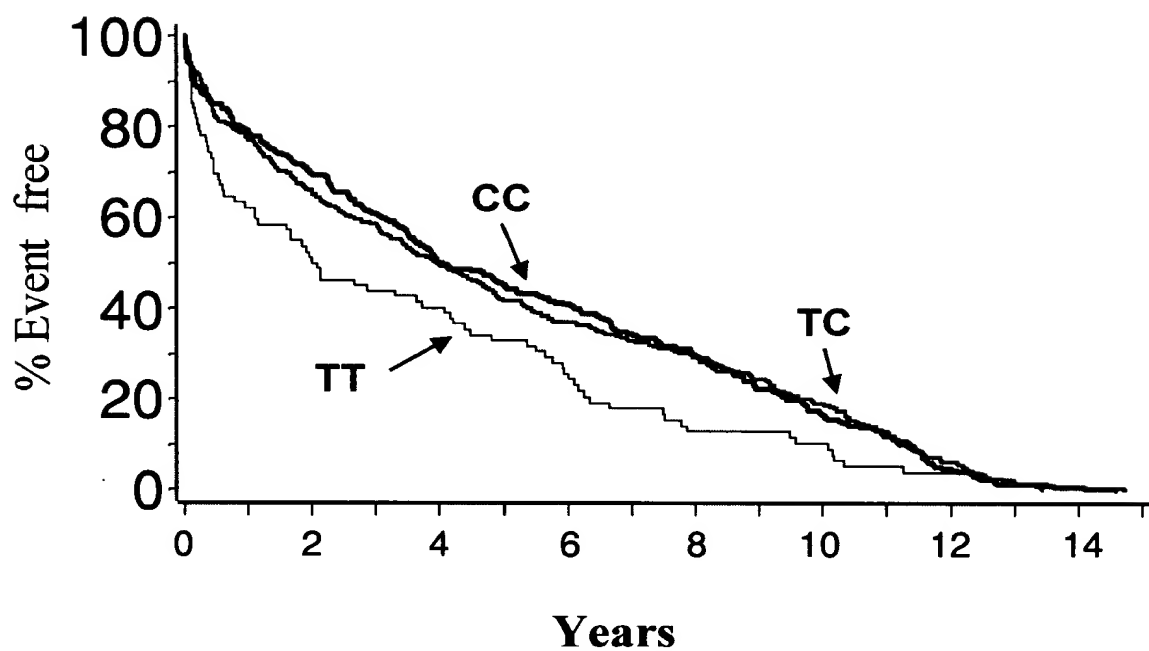




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FIG. 11

**Event: Lowest CD4 Cell Count**



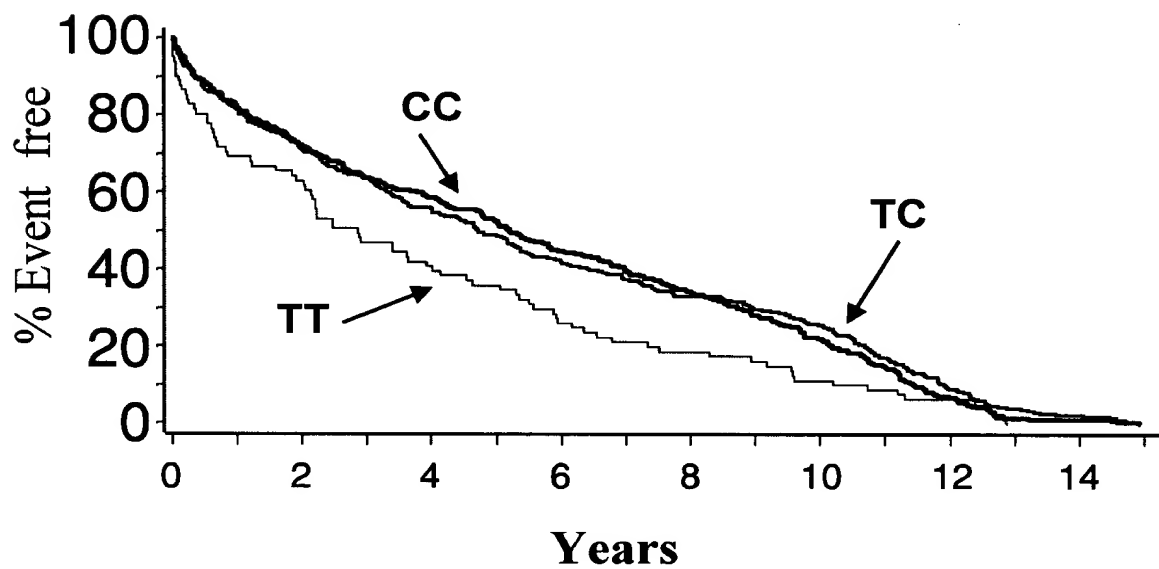


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FIG. 12

**Event: Time to maximum HIV Virus Load**

Virus Copy Number determined by Quantitative PCR





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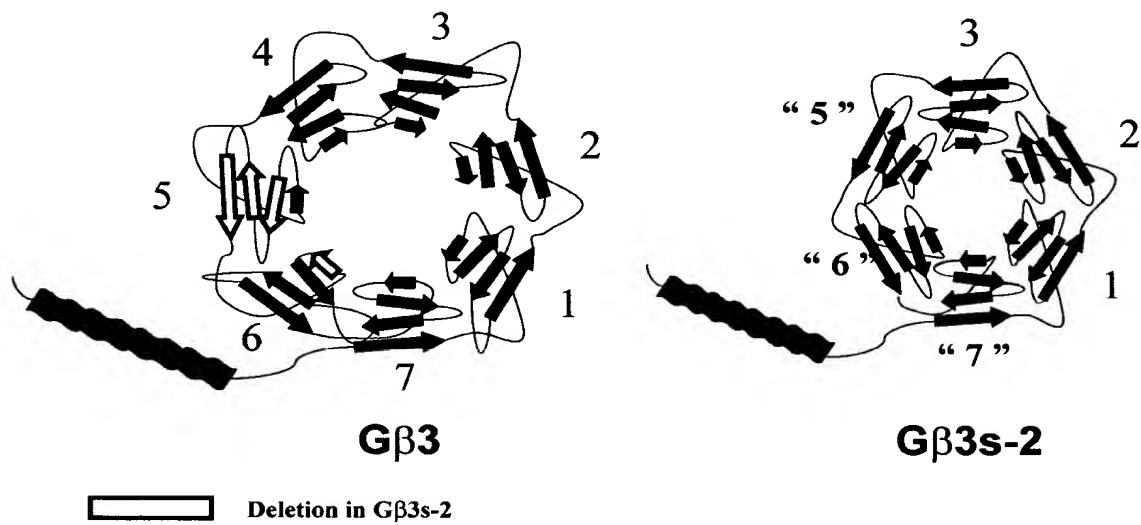
FIG. 13



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FIG. 14

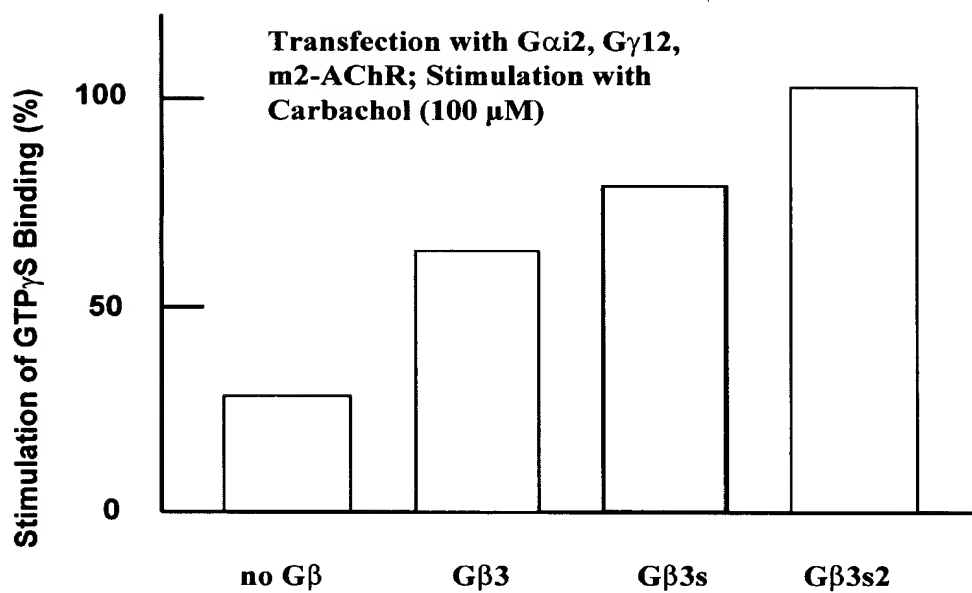
**Potential Structures of G $\beta$ 3 and G $\beta$ 3s / G $\beta$ 3s-2**





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FIG. 15





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FIG. 16

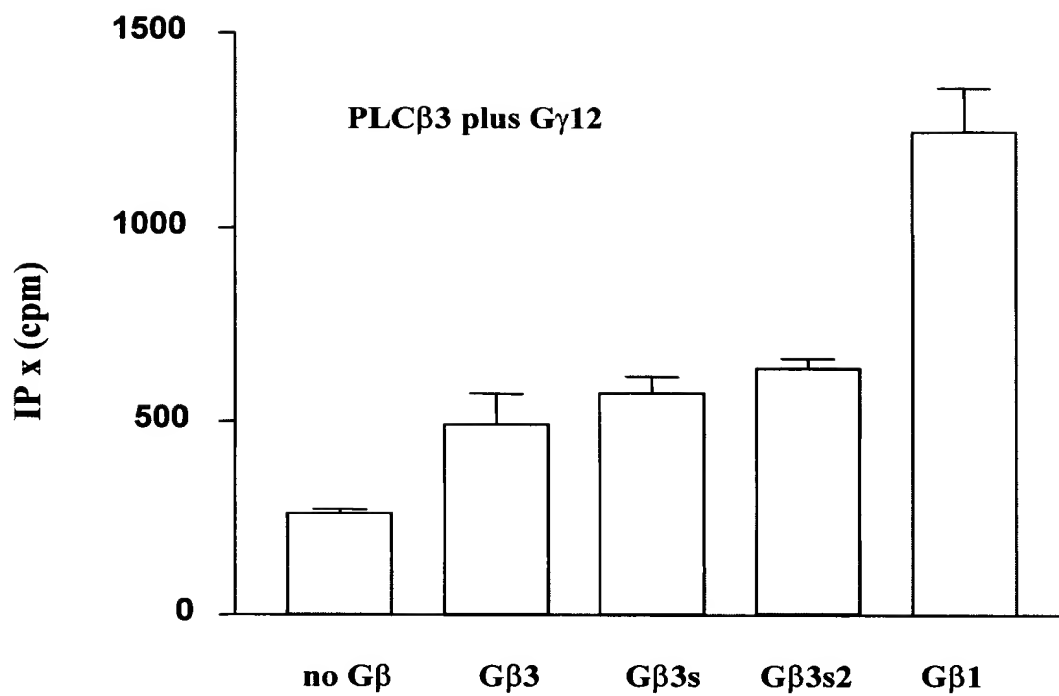






FIG. 17

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β3-original sequence of Levine. The exons are underlined alternately. The area which is omitted by cryptic splice as bold-faced.

- 1 gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT  
Start-ATG EXON 3 after Ansari-Lari  
Nucleotide 1-6 seem not to be affected
- 61 GCAGATGCCA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTC TGGCCTAGAG  
/Beginning EXON 4 /EXON 5 Beginning  
==> ENDE 1 KLON ANSARI
- 121 GTGGTGGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT  
EXON 5
- 181 TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG  
EXON 5 / Beginning EXON 6
- 241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCACT GCGCTCCTCC  
EXON 6 / EXON 7
- 301 TGGGTCATGA CCTGTGCTA TGCCCCATCA GGGAACTTTG TGGCATGTGG GGGGCTGGAC  
EXON 7
- 361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGGAG  
EXON 7
- 421 CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG  
EXON 7 /EXON 8
- 481 AACAGCTCGG GGGACACCAC GTGTGCCTTG TGGGACATTG AGACTGGGCA GCAGAAGACT  
EXON 8 /EXON 9  
cryptic SPLICING
- 541 GTATTTGTGG GACACACGGG TGA CTG CATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC  
EXON 9  
cryptic SPLICING
- 601 TTCATTTCCG GGGCCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC  
EXON 9  
cryptic SPLICING /
- 661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTTCTT CCCAATGGA  
EXON 9 / Beginning EXON 10
- 721 GAGGCCATCT GCACGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC  
EXON 10



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FIG. 17(cont.)

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCAGTC CGTGGCCTTC  
EXON 10 Polymorphism site acgtc tgt

841 TCCCTCAGTG GCCGCTACT ATTCGCTGGC TACGACGACT TCAACTGCAA TGTCTGGGAC  
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGGCCACG ATAACAGGGT GAGCTGCCTG  
EXON 10 /Beginning EXON 11

961 GGAGTCACAG CTGACGGGAT GGCTGTGGCC ACAGGTTCCT GGGACAGCTT CCTCAAAATC  
EXON 11

1021 TGGAAGTGAg gaggcctggag aaaggggaagt ggaaggcagt gaacacactc agcagcccc  
EXON 11  
End of Open Reading Frame

1081 tgcccgaccc catctcattc aggtgttctc ttctatattc cgggtgccat tccactaag  
EXON 11

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg  
EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccca cagtccctac  
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agccctttgc agggccagca  
EXON 11

1321 gacttgagtc tgaggcccca ggccttagga ttctctcccc agagccacta cctttgtcca  
EXON 11

1381 ggcctgggtg gtatagggcg tttggccctg tgactatggc tctggcacca ctagggtcct  
EXON 11

1441 ggccctcttc ttattcatgc tttctccttt ttctaccttt tttctctcc taagacacct  
EXON 11

1501 gcaataaagt gtagcaccct ggt  
EXON 11 POLY A SITE

"Ban Polymorphism"  
tctggcacta cta



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FIG. 18

Sequence with two polymorphisms (Numbering after the Levine sequence)

gggtogatgg	gggagatgga	gcaactgggt	caggaagogg	agcagctcaa	gaagcagatt	60
gcagatgoca	ggaaagoctg	tgctgaogtt	actctggcag	agctgggtgtc	tggoctagag	120
gtgggtgggac	gagtcagat	oggaogogg	oggaogtta	ggggacaocct	ggocaagatt	180
taogocatgc	actgggocac	tgattctaa	ctgctggtaa	gtgocctogca	agatgggaag	240
ctgatogtgt	gggacagcta	caaccaaac	aagggtgaog	ocatocact	gogctoctoc	300
tgggatcatga	octgtgoccta	tgoccatca	gggaactttg	tgcatgttg	ggggctggac	360
aacatgtgtt	ocatctacaa	octcaaatoc	ogtgaaggca	atgtcaagg	cagocgggag	420
ctttctgctc	acacaggtta	tctctoctgc	tgocgttoc	tgatgacaa	caatattgtg	480
aocagctogg	gggacaocac	gtgtgocctg	tgggacattg	agactgggca	gcagaagact	540
gtatttgtgg	gacacaoggg	tgactgcatg	agocgggtg	tgtctoctga	cttcaatctc	600
ttcatttogg	gggocgtgta	tgocagtgoc	aagctctggg	atgtgogaga	ggggaoctgc	660
ogtcagactt	tcactggoca	ogagtoggac	atcaaogoca	tctgtttctt	ccccaatgga	720
gaggocatct	gcaogggctc	ggatgaogct	toctgocgt	tgtttgaoct	gggggcagac	780
caggagctga	tctgcttctc	ocaogagagc	atcatctgog	gcatcaogtc	tgtggocctc	840
tooctcagtg	gocgocact	attogctggc	taogaogact	tcaactgcaa	tgtctgggac	900
tocatgaagt	ctgagogtgt	gggcatocctc	tcgggocag	ataacagggt	gagctgocctg	960
ggagtcacag	ctgaogggat	ggctgtggoc	acaggctoct	gggacagctt	octcaaaatc	1020
tggaactgag	gaggctggag	aaagggaggt	ggaaggcagt	gaacacactc	agcagoccc	1080
tgocogaac	catctcatctc	aggtgttctc	ttctatatctc	ogggtgocat	toocactaag	1140
ctttctoctt	tgagggcagt	ggggagcatg	ggactgtgoc	tttgggaggc	agcatcagg	1200
acacaggggc	aaagaactgc	occatctoct	occatggoc	tooctooca	cagtoctcac	1260
agocctctoc	ttaatgagca	aggacaocct	gocctoccc	agocctttgc	aggocagca	1320
gacttgagtc	tgaggoccca	ggocctagga	ttocctoccc	agagocacta	octttgtoca	1380
tctggcacta	ctaggocctg	gtggtatagg	gogtttggoc	ctgtgactat	ggctctggca	1440
ocactaggg	octggocctc	ttcttattca	tgctttctoc	ttttctaac	ttttttctc	1500
toctaagaca	octgcaataa	agtgtagcac	octggt			1536



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## FIG. 19

Nucleic acid sequence of cDNA of G $\beta$ 3 and description of the deletion in G $\beta$ 3 and G $\beta$ 3s-2. Numbering referenced to the cDNA of Levine et al. (Levine, M.A., Smallwood, P.M., Moen, P.T., Jr., Helman, L.J., and Ahn, T.G. Molecular cloning of  $\beta$ 3 subunit, a third form of the G protein beta-subunit polypeptide. *Proc.Natl.Acad.Sci USA* 87(6):2329-2333, 1990) Here numbering does not begin with start codon ATG, but 6 nucleotides earlier in the 5' area.

1 gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT

Start-ATG EXON 3

Nucleotide 1-6 seem not to be affected

61 GCAGATGCCA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTG TGGCCTAGAG

/Beginn EXON 4

/EXON 5 Beginning

121 GTGGTGGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT

EXON 5

181 TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCGCGCA AGATGGGAAG

EXON 5

/ Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCACT GCGCTCCTOC

EXON 6

/ EXON 7

301 TGGGTCATGA OCTGTGCGTA TGCCCCATCA GGGAACTTTG TGGCATGTGG GGGGCTGGAC

EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGGAG

EXON 7

421 CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG

EXON 7

/EXON 8

**Deletion bei G $\beta$ 3s**

481 ACCAGCTCGG GGGACACCAC GTGTGCCTTG TGGGACATTG AACTGGGCA GCAGAAGACT

EXON 8

/EXON 9

541 GTATTTGTGG GACACACGGG TGA CTG CATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC

EXON 9

601 TTCATTTTCGG GGGCCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC

EXON 9

**Deletion in G $\beta$ 3s2**

661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTTCTT CCCC AATGGA

EXON 9

/ Beginn EXON 10

Intron dazwischen 1607 bp



FIG. 19(cont.)

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**Deletion in G3s2**

721 GAGGCCATCT GCACGGGCTC GGATGACGCT TCTGCCGCT TGTITGACCT GCGGGCAGAC  
EXON 10

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCACGTC CGTGGGCTTC  
EXON 10 polymorphism site agtc tgt

841 TCCCTCAGTG GCGGCTACT ATTOGCTGGC TACGACGACT TCAACTGCAA TGTCTGGGAC  
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATOCTC TCTGGCCACG ATAACAGGGT GAGCTGCGTG  
EXON 10 /Beginning EXON 11 (Intron dazw. 989 bp)

961 GGAGTCACAG CTGACGGGAT GGCTGTGGCC ACAGGTTCTT GGGACAGCTT OCTCAAAATC  
EXON 11

1021 TGGAAGTGA gaggctggag aaaggggaagt ggaaggcagt gaacacactc agcagccccc  
EXON 11

End of Open Reading Frame B3-3

1081 tgcccgaccc catctcattc aggtgttttc ttctatatattc cgggtgccat tcccactaag  
EXON 11

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc ttggggaggc agcatcaggg  
EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccca cagtctcac  
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agccctttgc aggccagca  
EXON 11

1321 gacttgagtc tgaggcccca gggcctagga ttctctcccc agagccacta cttttgtcca  
EXON 11

**C1423T**

tctggcacta cta

1381 ggcctgggtg gtatagggcg tttggccctg tgactatggc tctggcacta ctagggtcct  
EXON 11

1441 ggccctcttc ttattcatgc tttctccttt ttctaccttt tttctctcc taagacacct  
EXON 11

1501 gcaataaagt gtagcaccct ggt  
EXON 11 POLY A SITE



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## FIG. 20

Amino acid sequence of GB3s-2 (Combined production)

atg ggg gag atg gag caa ctg cgt cag gaa gcg gag cag ctc aag aag	48
Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Lys	
5 10 15	
cag att gca gat gcc agg aaa gcc tgt gct gac gtt act ctg gca gag	96
Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu Ala Glu	
20 25 30	
ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg acg cgg	144
Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg	
35 40 45	
cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac tgg gcc	192
Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala	
50 55 60	
act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag ctg atc	240
Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile	
65 70 75 75	
gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca ctg cgc	288
Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg	
80 85 90	
tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac ttt gtg	336
Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val	
95 100 105	
gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc aaa tcc	384
Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser	
110 115 120	
cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac aca ggt	432
Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly	
125 130 135	
tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg acc agc	480
Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser	
140 145 150 155	



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FIG. 20(cont.)

tcg ggg gac acc acg tgt gcc ttg tgg gac att gag act ggg cag cag	528
Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln	
160 165 170 175	

aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg gct gtg	576
Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val	
180 185 190	

tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc agt gcc	624
ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala	
195 200 205	

aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc act ggc	672
Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly	
210 215 220	

cag gag tcg gac atc aac gcc atc tgt ttc ttc tcc ctc agt ggc cgc	720
His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Ser Leu Ser Gly Arg	
225 230 235	

cta cta ttc gct ggc tac gac gac ttc aac tgc aat gtc tgg gac tcc	768
Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser	
240 245 250 255	

atg aag tct gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg	816
Met Lys Ser Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val	
260 265 270	

agc tgc ctg gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc	864
Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser	
275 280 285	

tgg gac agc ttc ctc aaa atc tgg aac tga	894
Trp Asp Ser Phe Leu Lys Ile Trp Asn ***	
290 295	